

WO 00/24884

PCT/EP99/08323

1/7

Fig.1.

```

PstI
1  CAGGTCAGCTCAGGAGT CAGGGGAGGCTTGTGCAGGCTGGGGAGTCTCTGAACTCTCTCTGTGACGCTCTGGAAACACCTTCAGT
    +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
90  GTCCAGCTCAGGTCCTCAGTCCCTCCGAAACAGCTCGACCCCTCAGAGACTTTCAGAGGACAGCTCCGGAGACCTTTGTGGAGTCA
    +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
    Q V Q L Q E S G G L V Q A G E S L K L S C A A S G N T F S
    [-> CDR I

KpnI
91  GGCGGTTTCATGGGCTGTACCCGAGCTCCAGGAGCAGCGCGAGTTGGTCGACACCATTAATAGTAGAGGTATCAAACTATGCA
    +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
    CCGCCAAGTACCGACCATGGCGGTCGAGGTCCTTCTCGCGCTCAACGAGCTTGGTAATTATCATCTCCATAGTGTTCGTATAGT
    +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
    G G F M G W Y R Q A P G K Q R E L V A T I N S R G I T N Y A
    [-> CDR II

EagI
181 GACTCGTGAAGGCGGANTCACCATCTCCAGAGCAATGCCAAGAAGACAGTGTATTTGGAAATGACAGCCTGGACCTGAAGACAG
    +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
    CTGAGCACTCCCGGCTAAGTGTAGAGGTCCTGTTACGGTCTTCTGTACATTAACCTTTACTTTCGGACCTTGGACTTCGTGTC
    +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
    D F V K G R F T I S R D N A K K T V Y L E M N S L E P E D T
    [-> CDR III

BstEII
271 GCCGTTTATTACTGTATCACTCACTACTTCAGATCCTACTTGGGCTCAGGGGACCCAGGTCAACGCTCACGCTCTCTCTCA
    +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
    CGGCATATATGCAATGTGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGT
    +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
    A V Y Y C Y T H Y F R S Y W G Q G T Q V T V S S
    [-> CDR III
  
```

WO 00/24884

PCT/EP99/08323

27

Fig. 2.

1759

1 CAGGTGCACCTGCAGGAGTCAAGGGGAGGATTTGGTTCACAGCGGGGGGCTCTCTGAGACTCTCTCTGTGCAGGCTCTGCACGACCGCGAGT 90

GTCCAGTCGAGCTCTCAGTCCCTCTTACCAAGCTCCGCCCCGAGAGACTCTGAGAGGACACGTCGAGACCTGCGTGGCCCTCA
Q V O L Q E S G G G L V Q A G G S L R L S C A A S G R T G S

91 ACCTATGACATGGGCTGTTCCGCCAGGCTCCAGGGAAGGAGCGTGATCTGTAGCAGCTATTAACTGGGATAGTGCGCGGCACATACTAT 180

TGCATCTCTACCCGACGACGGCGTCCGACGCTCGACCTCAGACACATGGTCGATATTCAGCCCTATCAGCGCGGTATGATA
 T T Y D M G W F R Q A P G K E R E S V A A I N W D S A R T Y Y CDR II
 1-> CDR I <-1 1->

CDR II
EaqI

GCAAGCTCCGTGAGGGCCGATTCAACCATCTCCAGAGACAACGCCAAGAAGACGGTGTATCTGCAATGAACAGCCCTGAACCTGAGGAC

CGTTGAGGCACATCCCGGGCTAAGTGTAGAGTCCTCTGTGGGGTCTCTTGCCCAATAGACGTTTTACTTCTCGCATCTTTGGACTCCTG

A S S V R G R F T I S R R D N A K K T V Y L Q M N S L K P E D
 <-1

BsterI

ACGGCCGTTTATACCTGTGGCGCGGGGAAGGTGGTACTTGGGACTCCTGGGCCAGGGGACCAGGTCACCGTCTCCTCA

[illegible]

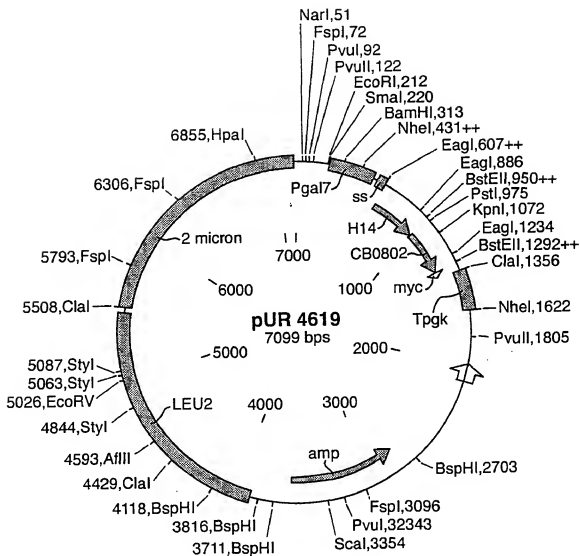
TGCCGGCAATATGGACACCGGCCCCCTTCCACCATGAACCTGAGGACCCCGGTCCCTGGGTCCAGTGGCAGAGGAGT

T A V Y T C G A G E G G T W D S W G Q G T Q V T V S S
1-> CDR III <-1

1->	CDR III	<-1
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
34	34	34
35	35	35
36	36	36
37	37	37
38	38	38
39	39	39
40	40	40
41	41	41
42	42	42
43	43	43
44	44	44
45	45	45
46	46	46
47	47	47
48	48	48
49	49	49
50	50	50
51	51	51
52	52	52
53	53	53
54	54	54
55	55	55
56	56	56
57	57	57
58	58	58
59	59	59
60	60	60
61	61	61
62	62	62
63	63	63
64	64	64
65	65	65
66	66	66
67	67	67
68	68	68
69	69	69
70	70	70
71	71	71
72	72	72
73	73	73
74	74	74
75	75	75
76	76	76
77	77	77
78	78	78
79	79	79
80	80	80
81	81	81
82	82	82
83	83	83
84	84	84
85	85	85
86	86	86
87	87	87
88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

CDR III

Fig.3.



WO 00/24884

PCT/EP99/08323

4/7

Fig.4.

XhoI
 1 CTGAGTCAGGGGAGGATTGGTCGAGCGGGGGGCTCTCTGAGACTCTCTGTGAGCCTCTGGAGCGACCGGAGTACGTATGACATG
 90
 GAGCTCAGTCCCTCTTAACACAGCTCCGGCCCGGAGAGACTCTGAGGAGACACTCGGAGACCTCGCTGGCGGCTCATGCACTGTGAC
 L E S G G G L V Q A G G S L R L S C A A S G R T G S T Y D M
 1-> CDR I
 GGCCTGTTCCGCCAGGCTCCAGGAGAGGCGTGAGTCTGTAGCAGCTATTACTGGGATAGTGGCGCACATCTATGCCAAGCTCCGTC
 91
 CGACCAAGCGGTCGAGGTCCCTTCTCGCACTCAGACATCGTGTGATATGACCTATCAGCGCGTGTATGATACGTTCGAGGCAC
 G W, F R Q A P G K E R E S V A A I N W D S A R T Y Y A S S V
 181
 CDR II
 1->
 AGGGCCGATTCCACCATCTCCAGAGACAACGCCAAGACGGTGTATCTGCAATGACACCTGAGACACCGGCCGTTTAT
 270
 TCCGGGCTAAGTGTAGAGTCTCTGTGGGTTCTTCTGCCACATAGAGCTTACTTGTGGACTTTGGACTCTCTGTGGCGGCAATA
 R G R F T I S R D N A K K T V Y L Q M N S L K P E D T A V Y
 <-1
 BstEII ↓ PstI
 271 ACCTGTGGCGGGGAGGTGTACTTTGGGACTCTCTGGGCCAGGGGACCCAGGTACACCTCTCTCAGGTGCAGCTGCAGAGTCA
 360
 TGGACACCGGCCCTTCCACCATGACCTGTAGGACCCCGGTCCCTGTGGTCCAGTGGCAGAGGAGTGTCCACGTGCAGGCTCTCAGT
 T C G A G E G G T W D S W G Q G T Q V T V S S Q V Q L Q E S
 1-> CDR III
 <-1

SUBSTITUTE SHEET (RULE 26)

WO 00/24884

PCT/EP99/08323

5/7

Fig. 4(Cont.)

361
GGGGAGGCTTGGTGCAGGCTGGGGAGTCTTGAACTCTCTGTGCGAGCTCTGGAAACACCTTCAGTGGCGGCTTCATGTGGGTGGTAC
KpnI
+-----+
CCCTCCGACCACTGCGACCCCTCAGACCTTTGAGAGACAGCTCGGAGACCTTTGTGGAGTCAACGCCGAGATCAACCGACCATG
GGGLVQAEGESLKLSCAASGNTFSGFGMGWY
+-----+
1--> CDR I <-1

341
CGCAGGCTCCAGGAGCAGCGGAGTTGGTGCACCATTAATAGTAGGTATCACAACTATGACACTTCGTGAGGGCGGATTC
+-----+
GGGTCCGAGGTCCCTTCGTGCGCTCAACAGCGTGTGTAATATCATCTCCATAGTGTGTGATAGCTGTGAAGCACTTCGCCGCTAAG
RQAPGKKQRELVATINSRGITNYADFVKGRF
+-----+
1-> CDR II <-1

341
EagI
ACCATCTCCAGACATCCAGAGACAGTATTTGGATGATGACAGCTGAGACAGCGCGTTTATTCTGTGTACCT
+-----+
TGGTAGAGTCTCTGTACGGTCTTCGTCAATACACTTTACTTCGGACCTTGGACTTCGTGCGCGCAATTAATGACATCTGA
TISRDNAKKTVYLEMNSSLEPEDTAVYCYT
+-----+
630

631
BstEII
CACTACTTCAGATCTACTGGGGTCAGGGGACCCAGGTCAAC
+-----+
672
GTGATGAGCTTAGGATGACCCAGTCCCTCGGTCAGTGG
HYFRSYWGGQTQVT
+-----+
1-> CDR III <-1

SUBSTITUTE SHEET (RULE 26)

Fig.5.

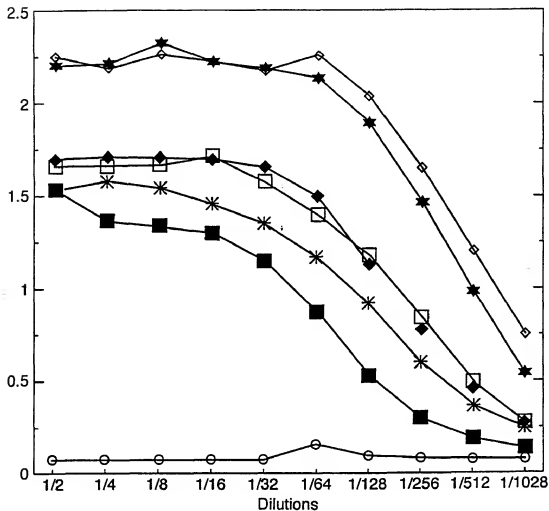


Fig.6.

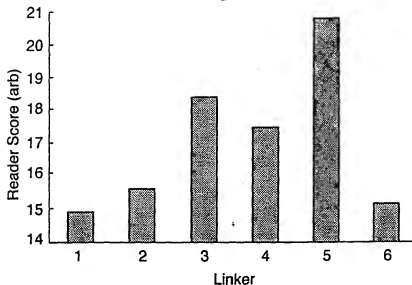


Fig.7.

